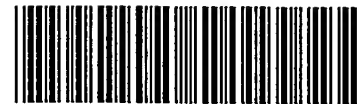


RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/530,987
Source: PCF
Date Processed by STIC: 5/18/06

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DATE: 05/18/2006

PATENT APPLICATION: US/10/530,987

TIME: 10:05:44

Input Set : A:\50125.101001.txt

Output Set: N:\CRF4\05182006\J530987.raw

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3 <110> APPLICANT: Dreher, Ingeborg
4     Moll, Thomas
6 <120> TITLE OF INVENTION: Antagonists IL-15
8 <130> FILE REFERENCE: 50125/101001
10 <140> CURRENT APPLICATION NUMBER: 10/530,987
11 <141> CURRENT FILING DATE: 2005-04-12
13 <150> PRIOR APPLICATION NUMBER: PCT/CH2003/00666
14 <151> PRIOR FILING DATE: 2003-10-13
16 <150> PRIOR APPLICATION NUMBER: EP 02022869.8
17 <151> PRIOR FILING DATE: 2002-10-14
19 <160> NUMBER OF SEQ ID NOS: 30
21 <170> SOFTWARE: PatentIn version 3.3
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24 <211> LENGTH: 114
25 <212> TYPE: PRT
26 <213> ORGANISM: Homo sapien
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34 Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
35             20             25             30
38 Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
39             35             40             45
42 Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
43 50             55             60
46 Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
47 65             70             75             80
50 Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
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55             100            105            110
58 Thr Ser
62 <210> SEQ ID NO: 2
63 <211> LENGTH: 231
64 <212> TYPE: PRT
65 <213> ORGANISM: Homo sapien
67 <400> SEQUENCE: 2
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70 1             5             10             15
73 Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
74             20             25             30
77 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
78             35             40             45

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81 Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
82      50              55              60
85 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
86 65      70              75              80
89 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
90      85              90              95
93 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
94      100             105             110
97 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
98      115             120             125
101 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
102      130             135             140
105 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
106 145      150             155             160
109 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
110      165             170             175
113 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
114      180             185             190
117 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
118      195             200             205
121 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
122      210             215             220
125 Leu Ser Leu Ser Pro Gly Lys
126 225             230
129 <210> SEQ ID NO: 3
130 <211> LENGTH: 232
131 <212> TYPE: PRT
132 <213> ORGANISM: Mus musculus
134 <400> SEQUENCE: 3
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140 Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile
141      20              25              30
144 Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val
145      35              40              45
148 Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val
149      50              55              60
152 Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp
153 65      70              75              80
156 Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln
157      85              90              95
160 Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp
161      100             105             110
164 Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val
165      115             120             125
168 Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr
169      130             135             140
172 Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu
173 145      150             155             160

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176 Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr
177                               165                               170                               175
180 Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr
181                               180                               185                               190
184 Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr
185                               195                               200                               205
188 Ser Cys Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys
189                               210                               215                               220
192 Ser Phe Ser Arg Thr Pro Gly Lys
193 225                               230
196 <210> SEQ ID NO: 4
197 <211> LENGTH: 346
198 <212> TYPE: PRT
199 <213> ORGANISM: artificial sequence
201 <220> FEATURE:
202 <223> OTHER INFORMATION: fusion protein
204 <400> SEQUENCE: 4
206 Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Thr Glu Asp Leu Ile
207 1                               5                               10                               15
210 Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
211                               20                               25                               30
214 Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
215                               35                               40                               45
218 Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
219                               50                               55                               60
222 Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
223 65                               70                               75                               80
226 Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
227                               85                               90                               95
230 Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn
231                               100                              105                              110
234 Thr Ser Asp Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys
235                               115                              120                              125
238 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
239                               130                              135                              140
242 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
243 145                              150                              155                              160
246 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
247                               165                              170                              175
250 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
251                               180                              185                              190
254 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
255                               195                              200                              205
258 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
259                               210                              215                              220
262 Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
263 225                              230                              235                              240
266 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
267                               245                              250                              255

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Input Set : A:\50125.101001.txt

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270 Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
271          260          265          270
274 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
275          275          280          285
278 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
279          290          295          300
282 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
283 305          310          315          320
286 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
287          325          330          335
290 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
291          340          345
294 <210> SEQ ID NO: 5
295 <211> LENGTH: 347
296 <212> TYPE: PRT
297 <213> ORGANISM: artificial sequence
299 <220> FEATURE:
300 <223> OTHER INFORMATION: fusion protein
302 <400> SEQUENCE: 5
304 Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Thr Glu Asp Leu Ile
305 1          5          10          15
308 Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
309          20          25          30
312 Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
313          35          40          45
316 Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
317          50          55          60
320 Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
321 65          70          75          80
324 Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
325          85          90          95
328 Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn
329          100          105          110
332 Thr Ser Asp Pro Arg Gly Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys
333          115          120          125
336 Cys Pro Ala Pro Asn Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro
337          130          135          140
340 Pro Lys Ile Lys Asp Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr
341 145          150          155          160
344 Cys Val Val Val Asp Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser
345          165          170          175
348 Trp Phe Val Asn Asn Val Glu Val His Thr Ala Gln Thr Gln Thr His
349          180          185          190
352 Arg Glu Asp Tyr Asn Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile
353          195          200          205
356 Gln His Gln Asp Trp Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn
357          210          215          220
360 Asn Lys Asp Leu Pro Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys
361 225          230          235          240

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Input Set : A:\50125.101001.txt

Output Set: N:\CRF4\05182006\J530987.raw

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364 Gly Ser Val Arg Ala Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu
365          245          250          255
368 Glu Met Thr Lys Lys Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe
369          260          265          270
372 Met Pro Glu Asp Ile Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu
373          275          280          285
376 Leu Asn Tyr Lys Asn Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr
377          290          295          300
380 Phe Met Tyr Ser Lys Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg
381 305          310          315          320
384 Asn Ser Tyr Ser Cys Ser Val Val His Glu Gly Leu His Asn His His
385          325          330          335
388 Thr Thr Lys Ser Phe Ser Arg Thr Pro Gly Lys
389          340          345
392 <210> SEQ ID NO: 6
393 <211> LENGTH: 341
394 <212> TYPE: DNA
395 <213> ORGANISM: Homo sapien
397 <400> SEQUENCE: 6
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400 attgatgcta ctttatatac ggaaagtgat gttcacccca gttgcaaagt aacagcaatg      120
402 aagtgccttc tcttgagatt acaagttatt tcacttgagt ccggagatgc aagtattcat      180
404 gatacagtag aaaatctgat catcctagca aacaacagtt tgtcttctaa tgggaatgta      240
406 acagaatctg gatgcaaaga atgtgaggaa ctggaggaaa aaaatattaa agaatttttg      300
408 cagagttttg tacatattgt ccaaagtgtc atcaacactt c              341
411 <210> SEQ ID NO: 7
412 <211> LENGTH: 697
413 <212> TYPE: DNA
414 <213> ORGANISM: Homo sapien
416 <400> SEQUENCE: 7
417 cccaaatctg ctgacaaaac tcacacatgc ccaccgtgcc cagcacctga actcctgggg      60
419 ggaccgtcag tcttcctctt cccccaaaaa cccaaggaca ccctcatgat ctcccgacc      120
421 cctgaggtca cgtgcgtggt ggtggacgtg agccacgaag accctgaggt caagttcaac      180
423 tggtagctgg acggcgtgga ggtgcataat gccaaagaaa agccgcggga ggagcagtac      240
425 aacagcacgt accgtgtggt cagcgtcctc accgtcctgc accaggactg gctgaatggc      300
427 aaggagtaca agtgcaaggt ctccaacaaa gccctcccag ccccatcga gaaaaccatc      360
429 tccaaagcca aagggcagcc ccgagaacca caggtgtaca ccctgcccc atcccgggat      420
431 gagctgacca agaaccaggt cagcctgacc tgccgtgtca aaggcttcta tcccagcgac      480
433 atcgccgtgg agtgggagag caatgggcag ccggagaaca actacaagac cagcctccc      540
435 gtgctggact ccgacggctc cttcttcctc tacagcaagc tcaccgtgga caagagcagg      600
437 tggcagcagg ggaacgtctt ctcatgctcc gtgatgcatg aggctctgca caaccactac      660
439 acgcagaaga gcctctccct gtctccgggt aaatgat              697
442 <210> SEQ ID NO: 8
443 <211> LENGTH: 700
444 <212> TYPE: DNA
445 <213> ORGANISM: Mus musculus
447 <400> SEQUENCE: 8
448 cccagagggc ccacaatcaa gccctgtcct ccatgcaaat gccagcacc taacctcttg      60
450 ggtggaccat ccgtcttcat cttccctcca aagatcaagg atgtactcat gatctccctg      120

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/530,987

DATE: 05/18/2006

TIME: 10:05:45

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